MSMLAERRRKQKWAVDPQNTAWSNDDSKFGQRMLEKMGWSKGKGLGAQEQGATDHIKVQ
VKNNHLGLGATINNEDNWIAHQDDFNQLLAELNTCHGQETTDSSDKKEKKSFSLEEKSK
ISKNRVHYMKFTKGKDLSSRSKTDLDCIFGKRQSKKTPEGDASPSTPEENETTTTSAFT
IQEYFAKPVAALKNKPQVPVPGSDISETQVERKRGKKRNKEATGKDVESYLQPKAKRHT
EGKPERAEAQERVAKKKCAPAEKQLRGPCWDQSSKASAQDAGDHVQPPEGRDFTLKPKK
RRGKKKLQKPVEIAEDATLEETLVKKKKKKDSK(328)

FIG. 1A

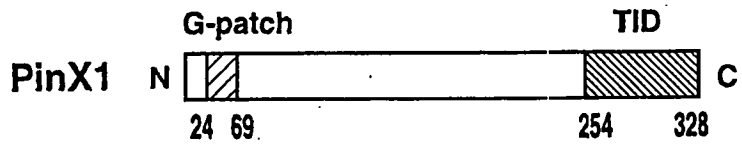


FIG. 1B

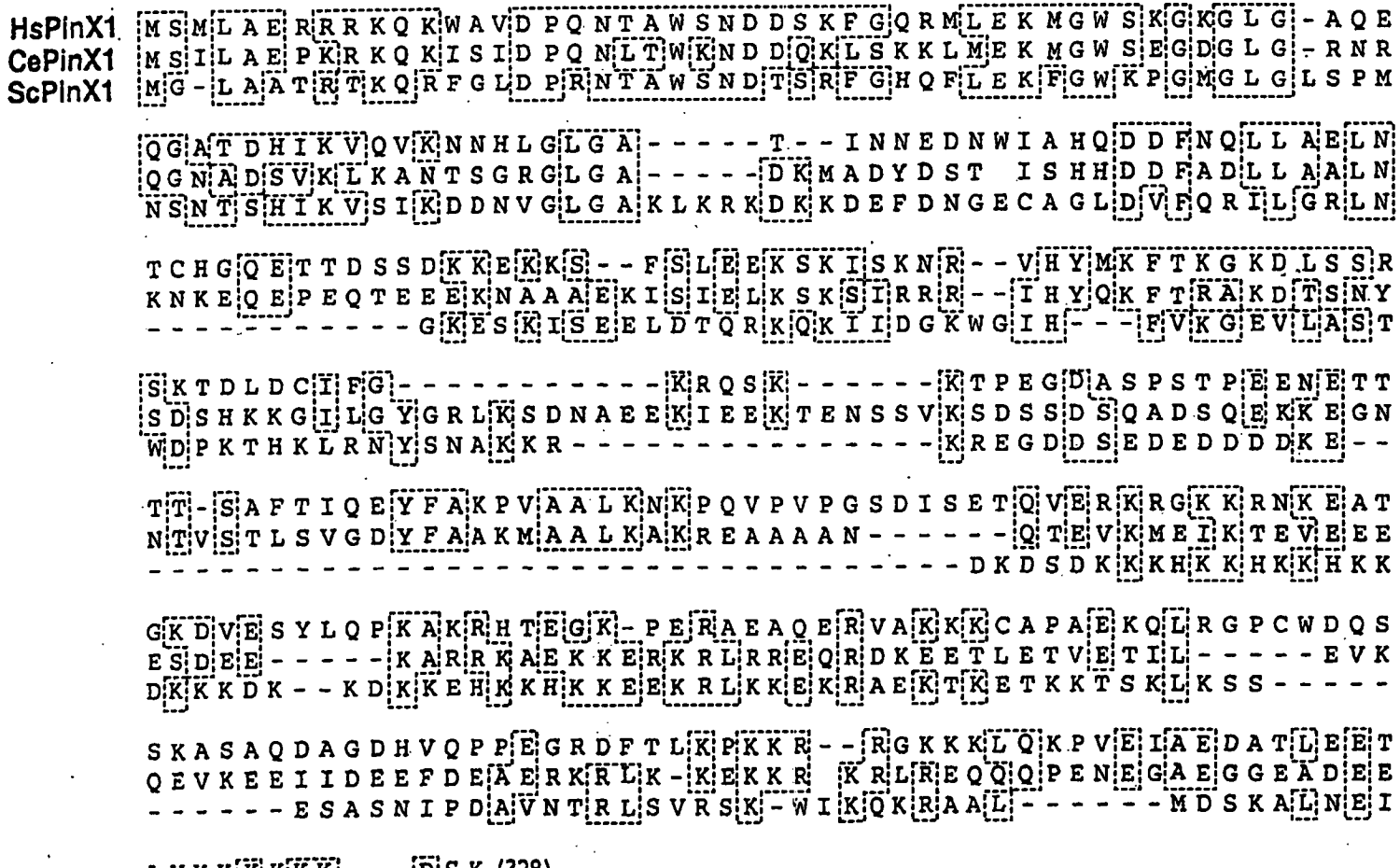


FIG. 1C

GCAGGAATTCGGCACGAGCTCCAGCCCGCCCAGTGGCCGCAGTCACCCAGGTCCAGAGGC
GGCGGTATCACAGGCTCTCCGACATGTCTATGCTGGCTGAACGTCGGCGGAAGCAGAAGTG
GGCTGTGGATCCTCAGAACACTGCCTGGAGTAATGACGATTCCAAGTTTGGCCAGCGGATG
CTAGAGAAGATGGGGTGGTCTAAAGGAAAGGGTTTAGGGGCTCAGGAGCAAGGAGCCACA
GATCATATTAAAGTTCAAGTGAAAAATAACCACCTGGGACTCGGAGCTACCATCAATAATGAA
GACAACTGGATTGCCCATCAGGATGATTTTAACCAGCTTCTGGCCGAACTGAACACTTGCCA
TGGGCAGGAAACCACAGATTCCTCGGACAAGAAGGAAAAGAAATCTTTTAGCCTTGAGGAAA
AGTCCAAAATCTCCAAAAACCGTGTTCACTATATGAAATTCACAAAAGGGAAGGATCTGTCAT
CTCGGAGCAAAACAGATCTTGACTGCATTTTTGGGAAAAGACAGAGTAAGAAGACTCCCGAG
GGCGATGCCAGTCCCTCCACTCCAGAGGAGAACGAAACCACGACAACCAGCGCCTTCACCA
TCCAGGAGTACTTTGCCAAGCCGGTGGCAGCACTGAAGAACAAGCCCCAGGTTCCAGTTCC
AGGGTCTGACATTTCTGAGACGCAGGTGGAACGTAAAAGGGGGAAGAAAAGAAATAAAGAG
GCCACAGGTAAAGATGTGGAAAGTTACCTCCAGCCTAAGGCCAAGAGGCACACGGAGGGAA
AGCCCGAGAGGGCCGAGGCCCAGGAGCGAGTGGCCAAGAAGAAGTGCGCGCCAGCAGAA
AAACAGCTCAGAGGCCCCTGCTGGGACCAGAGTTCCAAGGCCTCTGCTCAGGATGCAGGG
GACCATGTGCAGCCGCCTGAGGGCCGGGACTTCACCCTGAAGCCCAAAAAGAGGAGAGGG
AAGAAAAAGCTGCAAAAACCAGTAGAGATAGCAGAGGACGCTACACTAGAAGAAACGCTAG
TGAAAAAGAAGAAGAAGAAAGATTCCAAATGAATCCTTCCCAGCCGGGGCCTTCCGACCACT

FIG. 1D-1

FIG. 1D-1
FIG. 1D-2

FIG. 1D

CAGCTGTCAGGGCACTGCGGGGGCAGACACCTCTGGCCTGAAGTCACAGCAGAGTTCACC
CCAGAGCGCCTGGGCGCATCTTGTGGCATGCCCATGGGCTGCCGAGTCCTGCCCTCTCGC
CACATTTCCCCCAAGTTACATTCCCAGGAGGACCTTTTTAATGTTCTCAATCGTGGCTCTCAG
ACACAAATAAATTCTCGTGCCGAATTCGGCACGAGCTCGCTCTCATTCCTGATGTGGACATC
GACTCCGACGGCGTCTTCAAGTATGTGTTGATCCGAGTCCACTCGGCTCCCCGCTCCGGGG
CTCCGGCTGCAGAGAGCAAGGAGATCGTGCGCGGCTACAAGTGGGCTGAGTACCATGCGG
ACATCTACGACAAAGTGTCGGGCGACATGCAGAAGCAAGGCTGCGACTGTGAGTGTCTGGG
CGGCGGGCGCATCTCCCACCAGAGTCAGGACAAGAAGATTCACGTGTACGGCTATTCCATG
GCCTATGGTCCTGCCCAGCACGCCATTTCAACTGAGAAAATCAAAGCCAAGTACCCCGACTA
CGAGGTCACCTGGGCTAACGACGGCTACTGAGCACTCCCAGCCCGGGGCCTGCTGCCTCC
AGCAGCCACTTCAGAGCCCCCGCCTTTGCCTGCACTCCTCTTGCAGGGCTGGCCCTGCCTG
CTCCTGCGGCAGCCTCTGGTGACGTGCTGTCCACCAGGCCTTGGAGACAGGCTAGCCTGG
CCACAGAATTAAACGTGTTGCCACACCAAAAAAAAAAAAAAAAAAAA

coding regions:84 to 1070

Protein sequence:
MSMLAERRRKQKWAVDPQNTAWSNDDSKFGQRMLEKMGWSKGKGLGAQEQGATDHIKVQVKNNHLGLGATI
NNEDNWIAHQDDFNQLLAELNTCHGQETTDSSDKKEKKSFSLEEKSKISKNRVHYMKFTKGKDLSSRSKTD
LDCIFGKRQSKKTPEGDASPSTPEENETTTTSAFTIQEYFAKPVAALKNKPQVPVPGSDISETQVERKRGK
KRNKEATGKDVESYLQPKAKRHTEGKPERAEAQERVAKKKCAPAEKQLRGPCWDQSSKASAQDAGDHVQPP
EGRDFTLKPKKRRGKKKLQKPVEIAEDATLEETLVKKKKKKDSK

FIG. 1D-2

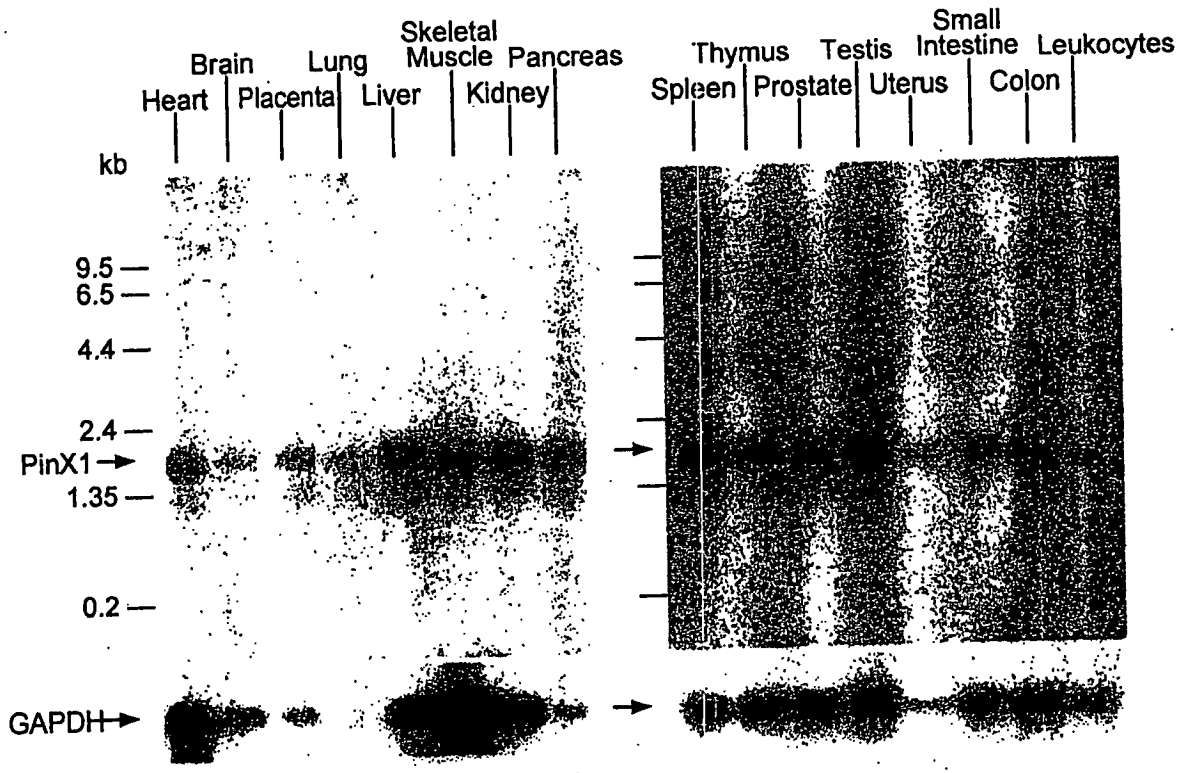

Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
Spleen
Thymus
Prostate
Testis
Uterus
Small Intestine
Colon
Leukocytes
kb
9.5
6.5
4.4
2.4
PinX1
1.35
0.2
GAPDH

FIG. 2A

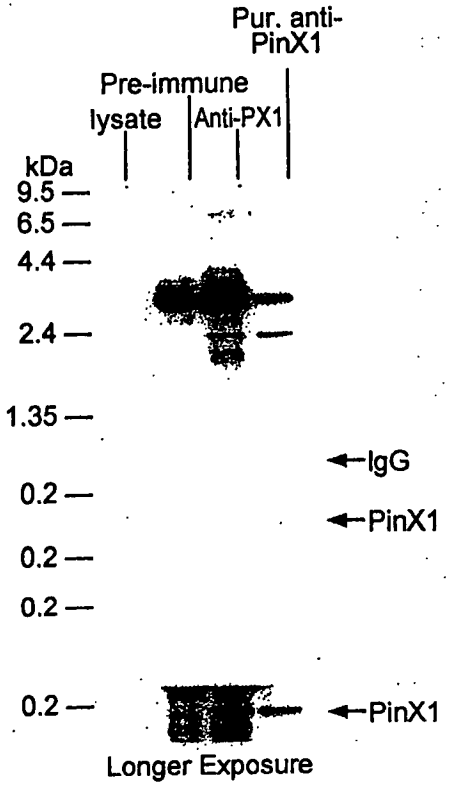


FIG. 2B

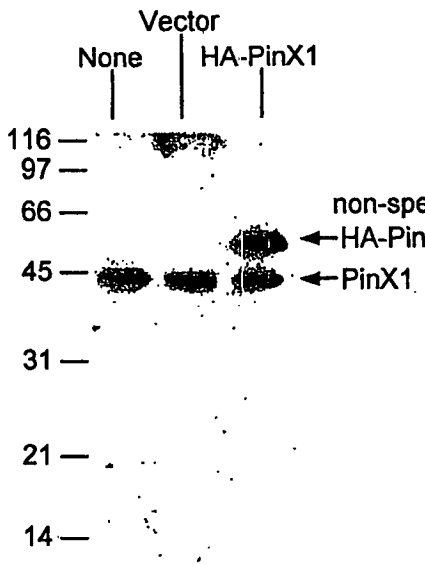


FIG. 2C

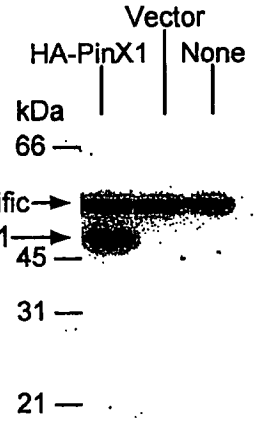


FIG. 2D

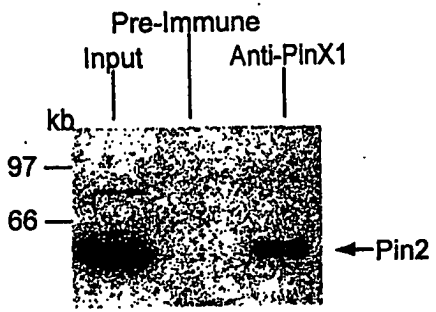

Pre-Immune
Input
Anti-PinX1
kb
97
66
Pin2

FIG. 3A

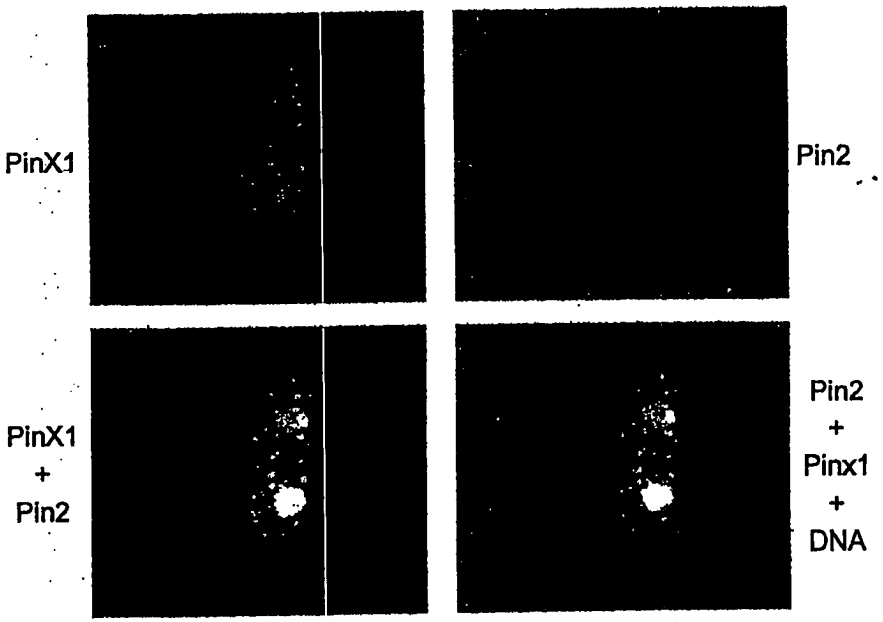

PinX1
Pin2
PinX1
+
Pin2
Pin2
+
Pinx1
+
DNA

FIG. 3B

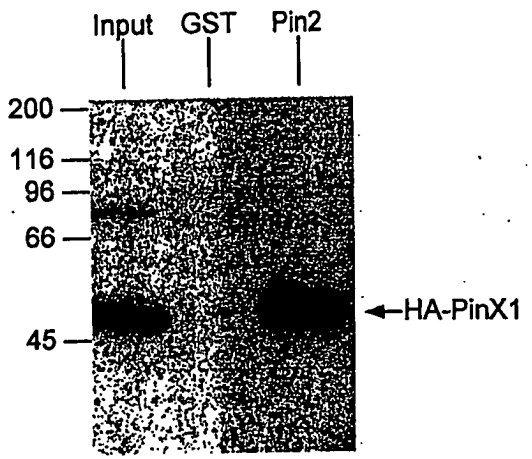

Input
GST
Pin2
200
116
96
66
45
HA-PinX1

FIG. 3C

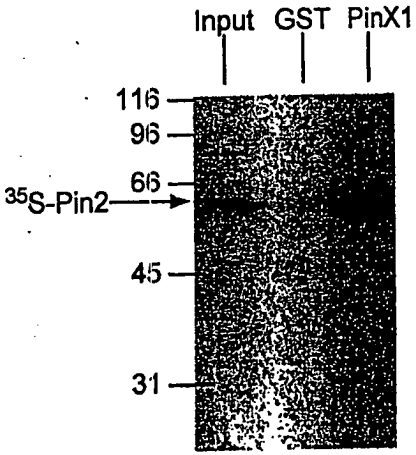

Input
GST
PinX1
116
96
66
35S-Pin2
45
31

FIG. 3D

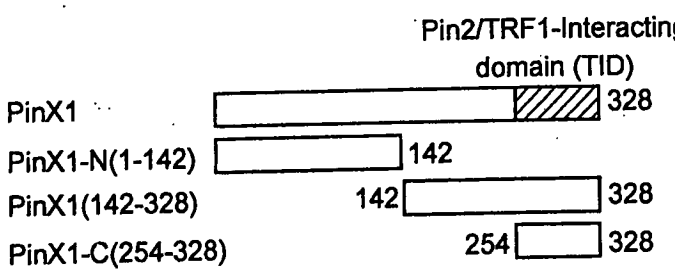

Pin2/TRF1-Interacting
domain (TID)
PinX1
328
PinX1-N(1-142)
142
PinX1(142-328)
142
328
PinX1-C(254-328)
254
328

FIG. 3E

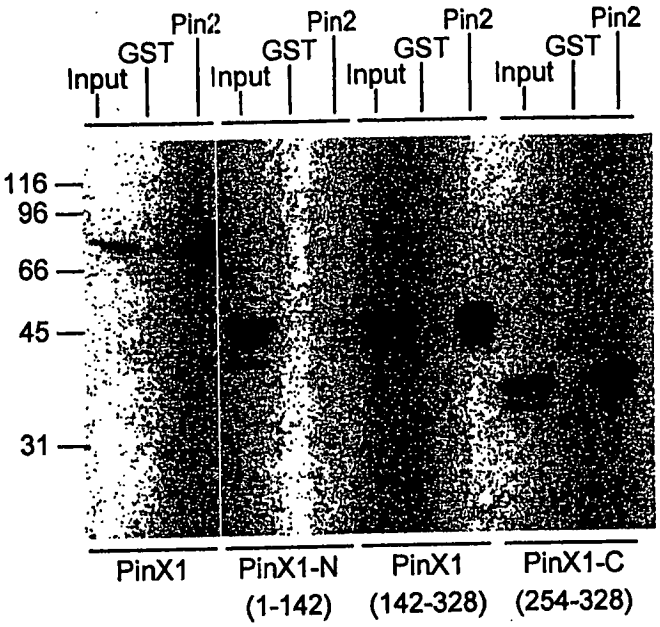

Input
GST
Pin2
Input
GST
Pin2
Input
GST
Pin2
Input
GST
Pin2
116
96
66
45
31
PinX1
PinX1-N
(1-142)
PinX1
(142-328)
PinX1-C
(254-328)

FIG. 3F

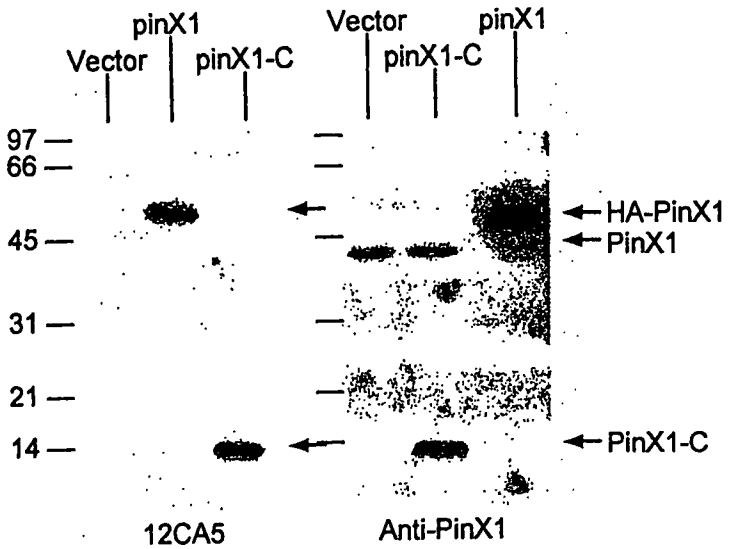

pinX1
Vector
pinX1-C
Vector
pinX1-C
pinX1
97
66
45
31
21
14
HA-PinX1
PinX1
PinX1-C
12CA5
Anti-PinX1

FIG. 4A

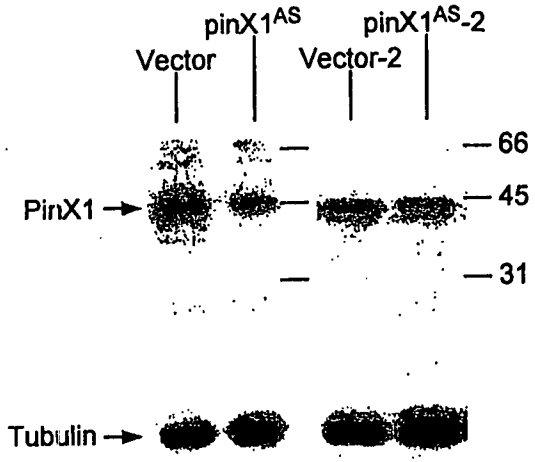

pinX1AS
pinX1AS-2
Vector
Vector-2
66
45
31
PinX1
Tubulin

FIG. 4B

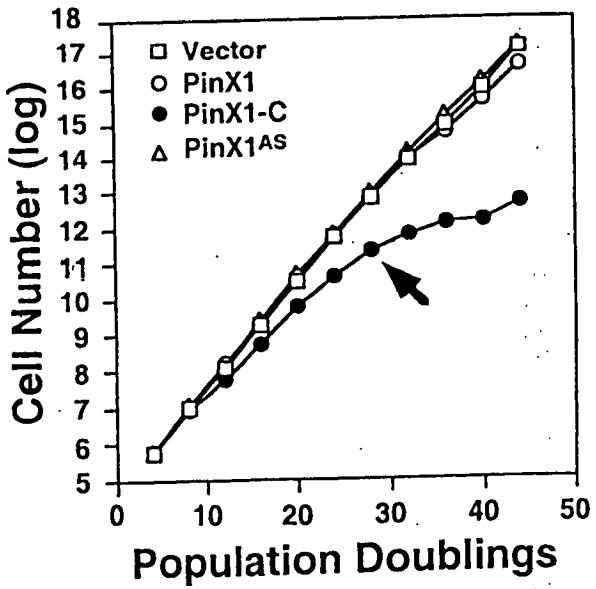

Cell Number (log)
Population Doublings
Vector
PinX1
PinX1-C
PinX1AS
18
17
16
15
14
13
12
11
10
9
8
7
6
5
0
10
20
30
40
50

FIG. 4C

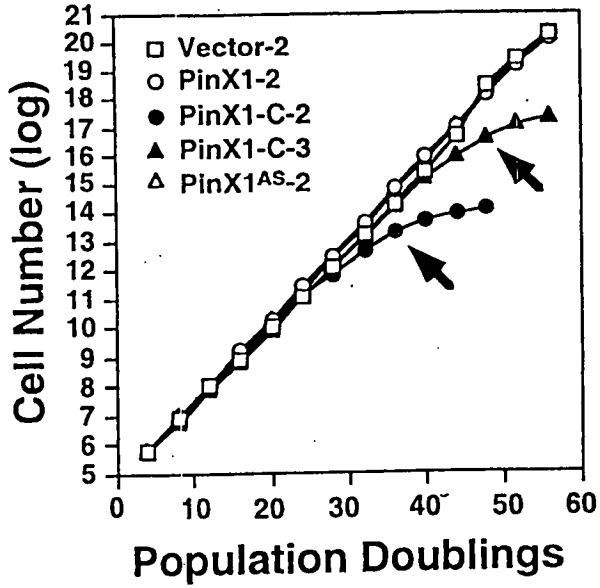

Cell Number (log)
Population Doublings
Vector-2
PinX1-2
PinX1-C-2
PinX1-C-3
PinX1AS-2
21
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
0
10
20
30
40
50
60

FIG. 4D

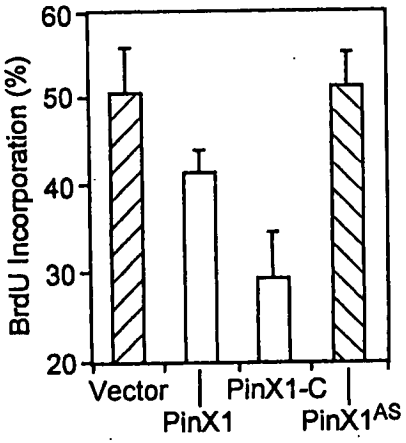


FIG. 5A

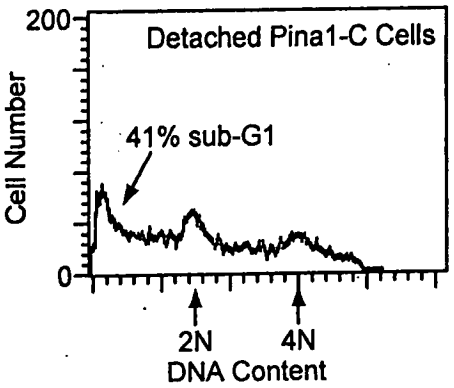


FIG. 5B

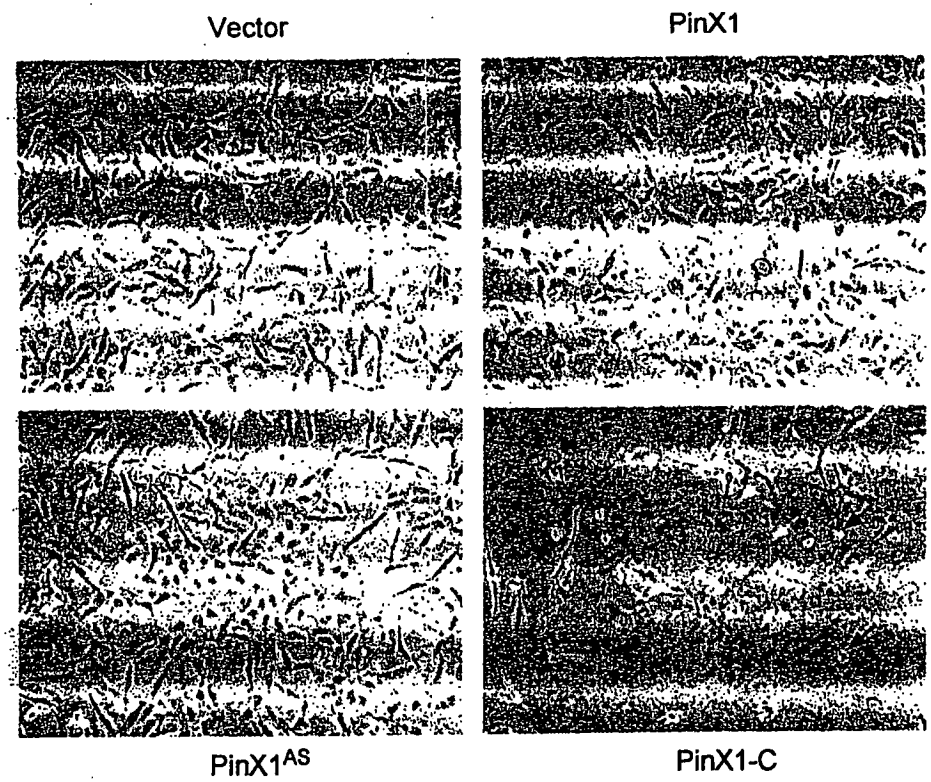


FIG. 5C

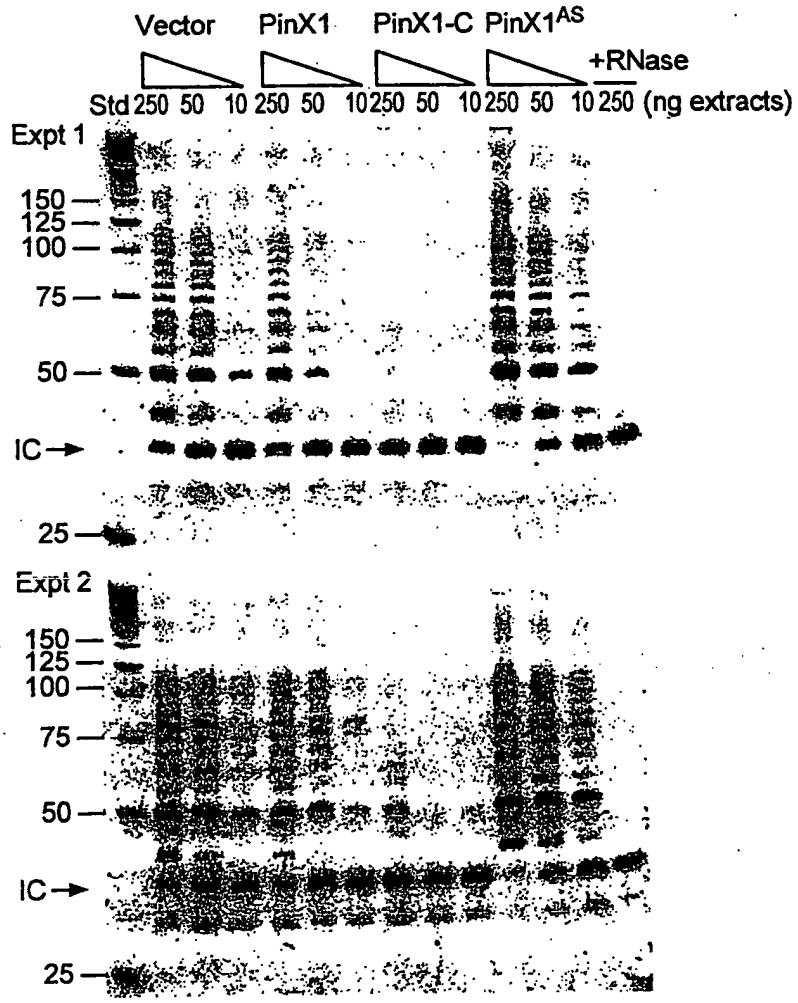

Vector
PinX1
PinX1-C
PinX1AS
+RNase
Std 250 50 10 250 50 10 250 50 10 250 50 10 250 (ng extracts)
Expt 1
150
125
100
75
50
IC
25
Expt 2
150
125
100
75
50
IC
25

FIG. 6A

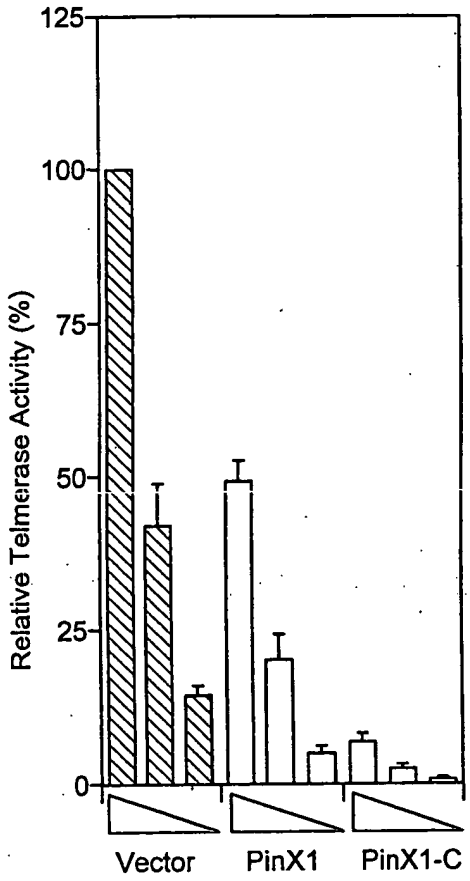


FIG. 6B-1

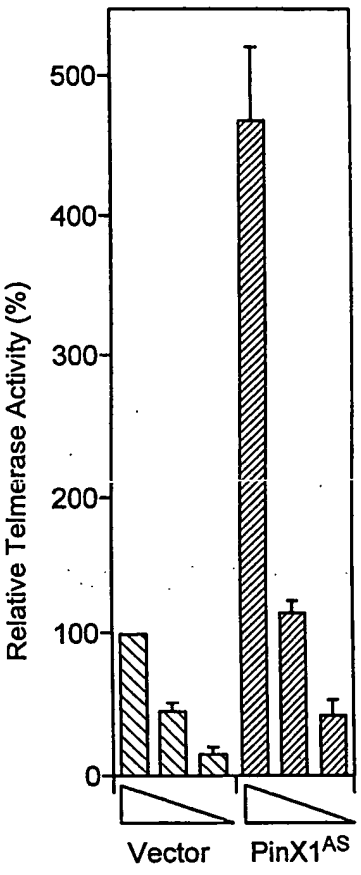


FIG. 6B-2

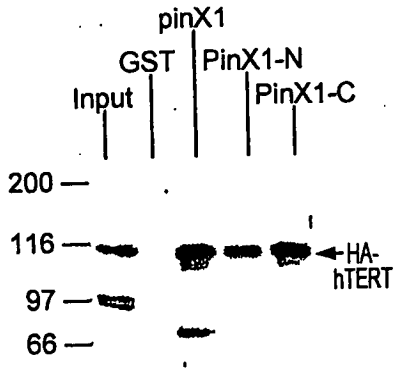


FIG. 7A

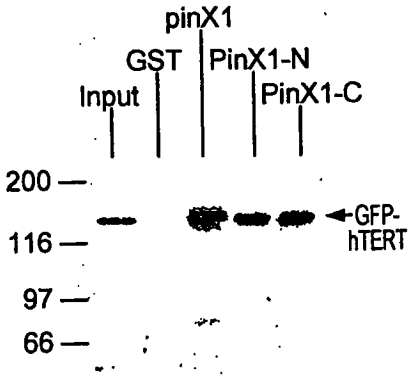


FIG. 7B

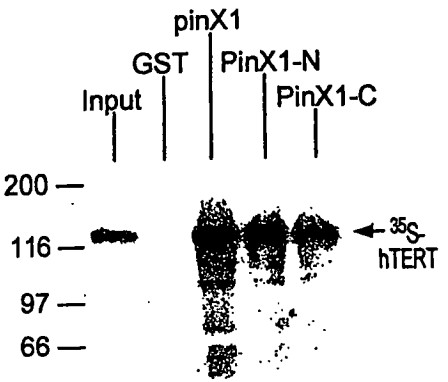


FIG. 7C

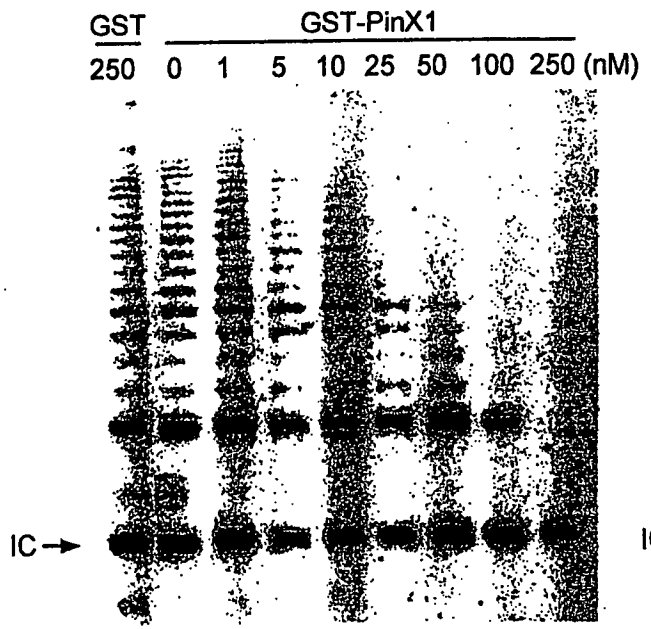

GST
GST-PinX1
250 0 1 5 10 25 50 100 250 (nM)
IC

FIG. 7D

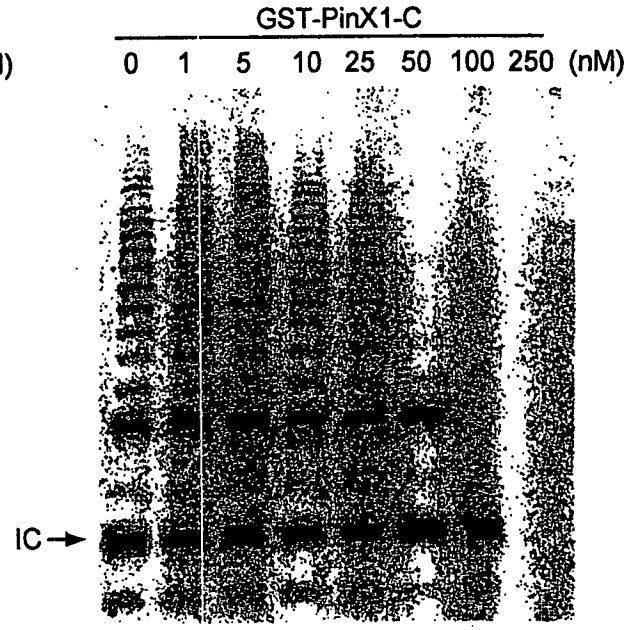

GST-PinX1-C
0 1 5 10 25 50 100 250 (nM)
IC

FIG. 7E

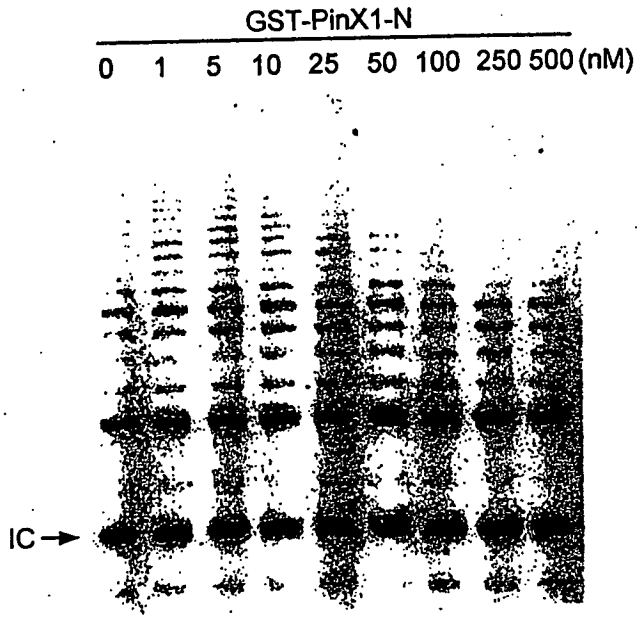

GST-PinX1-N
0 1 5 10 25 50 100 250 500 (nM)
IC

FIG. 7F

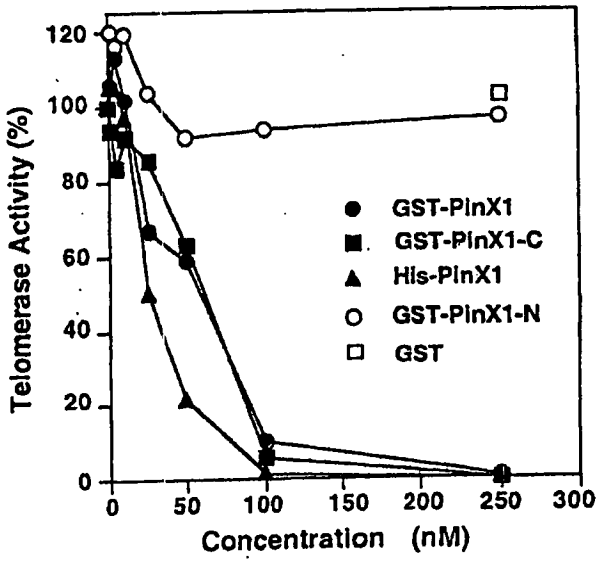

Telomerase Activity (%)
120
100
80
60
40
20
0
0 50 100 150 200 250 300
Concentration (nM)
GST-PinX1
GST-PinX1-C
His-PinX1
GST-PinX1-N
GST

FIG. 7G

Table 1. Functional Properties of Pinx1 and its Mutants

PinX1 Protein	Pin2/TRF1 Binding	hTERT Binding	Inhibition on Telomerase in vitro	Effect on Telomerase in Cells	Effect on Cell Growth in vivo
PinX1 (1 — TID — 328)	+	+	+	Partially inhibit	Partially inhibit
PinX1-N (1 — 142)	-	+	-	N.D.	N.D.
PinX1-C (TID) (254 — TID — 328)	+	+	+	Completely inhibit	Induce crisis
PinX1^{AS} "328" — "1"	N.A.	N.A.	N.A.	Increase	No affect

FIG. 8

Expression of PinX1 is decreased in some human tumor tissues as determined by immunostaining

Tissues	PinX1 Expression	
	Normal	Tumor
Liver	+	-
Breast	+	-
Kidney	+	-
Skin	+	-
Colon	+	-

FIG. 9

Depletion of PinX1 by expression of antisense PinX1 increases the tumorigenecity of HT1080 cells

HT1080 cell lines	Tumor Frequency	Tumor Weight (g)
Vector	2/5	0.05, 0.01
$PinX1^{AS}$	4/5	0.6, 1.0, 1.2, 3.5
PinX1	0/5	
PinX1-C	0/5	

FIG.10A

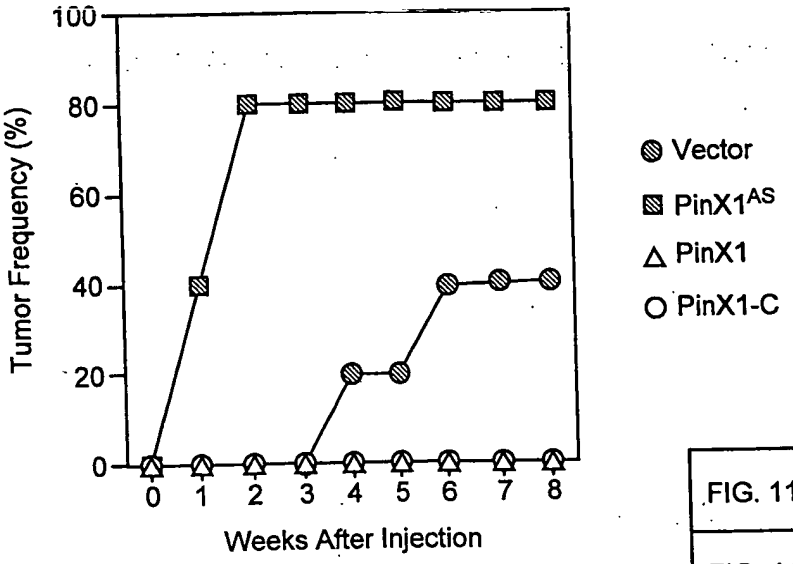


FIG.10B

FIG. 11A
FIG. 11B

FIG. 11

PinX1-L1 cDNA sequence (needed to be finally confirmed)

ATGTTGATGCTGGCTGAGCAGCAGCAGAAGCAGAAGTGGGCTGTGAATACTCAAAACACTG
CCTGGAGTAATGCTGATTCTAAATTTGGCCAGAGGATACTAGAGAAGATGGAATGGTCTAAA
GGAAGGGGTTTAGGGGTTCAGGAGCAAGGAGGCCCAGATGATATTAAAGTTCAAGTTAAAA
ATAACGACCTGGGACTTCAAGCTACAATCAATAATGAAGCCAACTGGATTGCCCATCAAGAT
GATTTTAACTGGCTTCTGGCGGAACTGAACACTTGTCAGAGGCAGGAAACAGCAGACTCCTT
AGACAACAAGAAAAAGAAATATTTTAGTCTTGAAGAAATTCCAAAATCTTCAAAAaACTGTGTT
CATCATAGGAAATTTACAAAAGAAAAGGATCTATCATCTCGGAGCAAAACAGATCGTGACTG
CATTTTTGGGAAAAAACAGAGTAAGAAGACTCCCGAGGGTAATTCCAGTCCCTCCACTCCAG
ACaAGAACAAAACCACGATGACAACCCATGCCTTCACCATCCAGGAGCGTTTTGCCAAGCGA
ATGGCAGCACTGAAGAACAAGCCCCAGGTTGCAGCTCCAGGGCCTGACATTTCCAAGACCC
AAGTGGAATGCAAAAGGGGGAAGAAAAGAAACAAAGAGGCAACAGGTAAAAATGGGGAGAG
TTACCCCCCAACACAGCCTAAGGCCAAGCGGCCTAAAGAGGGAAAGCCTAAGAGAGACAAG
GTCCAGAAGTCGGCATCCAAGGAGAAAAGAGCACGGACAGACGGACAGTGCAGAGGCCTC
TGCTGGGAAGAGAGTTCTGAGGCCTCTGCTCAGGGTGCAGGGAATTGTGTGCAGCCACCTG
ATGGCCAGGATTTCACCCTGAAGCCCAAAAAGACAAGAGGAAAAAAAAAAAGCTGCAAAGCC
AGTAGAGGTAGCAATGGACACTACGCTGAAAGAAACACCAATGAAAAATAAGAAAAAGAAGA
AAGGTTCCAAATGAATTCTCTCCAGCCAGGGCCTTCCGACCACTCAGCTTGTCAGGGCGCT
GCTGGGGCAGACACCTCTGGCCTGAAGTCAGAGCAGAGTTCACCCCAGAGAGCCGGGGCA
CATCTTGTGACATGCCTGTGGGTGGCCGAGTCTCGCCCTCTCACCACATTTCTCCCCAAGTT
ATGTTCCCAGGAGGGCTTTTTTTAAATGTTCTAAATCATGGCTTTCATAAACAAATACATTTTT
GTAA

FIG. 11A

PinX1-L1 peptide sequence (needed to be finally confirmed)

MLMLAEQQQKQKWAVNTQNTAWSNADSKFGQRILEKMEWSKGRGLGVQEQGGPDDIKVQVK
NNDLGLQATINNEANWIAHQDDFNWLLAELNTCQRQETADSLDNKKKKYFSLEEIPKSSKNCVH
HRKFTKEKDLSSRSKTDRDCIFGKKQSKKTPEGNSSPSTPDKNKTTMTTHAFTIQERFAKRMAAL
KNKPQVAAPGPDISKTQVECKRGKKRNKEATGKNGESYPPTQPKAKRPKEGKPKRDKVQKSAS
KEKRARTDGQCRGLCWEESSEASAQGAGNCVQPPDGQDFTLKPKKTRGKKKAAKPVEVAMDT
TLKETPMKNKKKKKGSK

FIG. 11B

Alignment Report of Untitled, using J. Hein method with PAM250 residue weight table.
Thursday, May 3, 2001 11:42 AM

```
     M . MLAE . . . KQKWAV . . QNTAWSN . DSKFGQR . LEKM . WS  Consensus #1
                  10        20        30        40
1    MSMLAERRRKQKWAVDPQNTAWSNDDSKFGQRMLEKMGWS  Pimx1-aa
1    MLMLAEQQQKQKWAVNTQNTAWSNADSKFGQRILEKMEWS  Pimx1-Llaa

     KG . GLG . QEQG . . D . IKVQVKNN . LGL . ATINNE . NWIAH  Consensus #1
                  50        60        70        80
41   KGKGLGAQEQGATDHIKVQVKNNHLGLGATINNEDNWIAH  Pimx1-aa
41   KGRGLGVQEQGGPDDIKVQVKNNDLGLQATINNEANWIAH  Pimx1-Llaa

     QDDFN . LLAELNTC . . QET . DS . D . K . KK . FSLEE . . K . S  Consensus #1
                  90        100       110       120
81   QDDFNQLLAELNTCHGQETTDSSDKKEKKSFSLEEKSKIS  Pimx1-aa
81   QDDFNWLLAELNTCQRQETADSLDNKKKKYFSLEEIPKSS  Pimx1-Llaa
```

FIG. 12A
FIG. 12B
FIG. 12C

FIG. 12

FIG. 12A

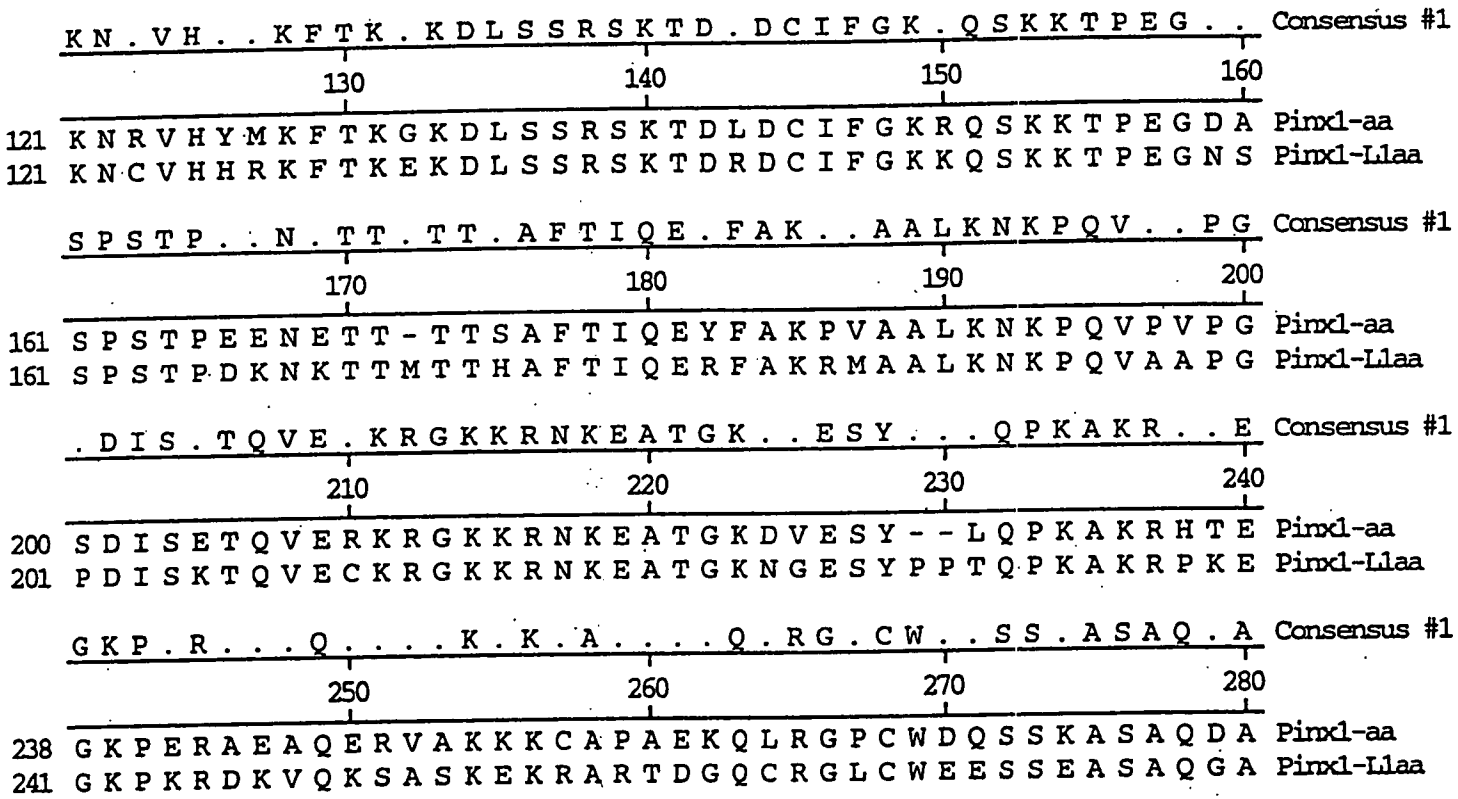
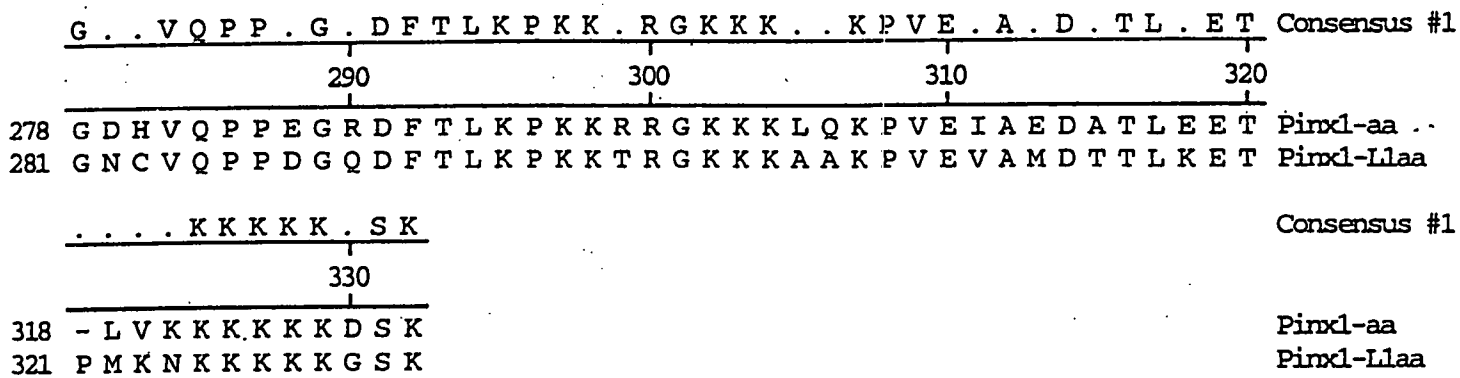
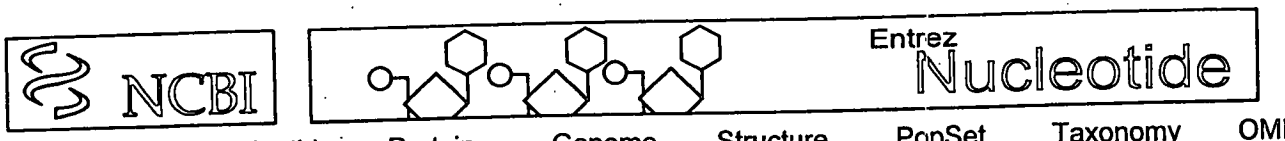

KN.VH..KFTK.KDLSSRSKTD.DCIFGK.QSKKTPEG.. Consensus #1
130 140 150 160
121 KNRVHYMKFTKGKDLSSRSKTDLDCIFGKRQSKKTPEGDA Pimx1-aa
121 KNCVHHRKFTKEKDLSSRSKTDRDCIFGKKQSKKTPEGNS Pimx1-Llaa
SPSTP..N.TT.TT.AFTIQE.FAK..AALKNKPQV..PG Consensus #1
170 180 190 200
161 SPSTPEENETT-TTSAFTIQEYFAKPVAALKNKPQVPVPG Pimx1-aa
161 SPSTPDKNKTTMTTHAFTIQERFAKRMAALKNKPQVAAPG Pimx1-Llaa
.DIS.TQVE.KRGKKRNKEATGK..ESY...QPKAKR..E Consensus #1
210 220 230 240
200 SDISETQVERKRGKKRNKEATGKDVESY--LQPKAKRHTE Pimx1-aa
201 PDISKTQVECKRGKKRNKEATGKNGESYPPTQPKAKRPKE Pimx1-Llaa
GKP.R...Q....K.K.A....Q.RG.CW..SS.ASAQ.A Consensus #1
250 260 270 280
238 GKPERAEAQERVAKKKCAPAEKQLRGPCWDQSSKASAQDA Pimx1-aa
241 GKPKRDKVQKSASKEKRARTDGQCRGLCWEESSEASAQGA Pimx1-Llaa

FIG. 12B



Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

FIG. 12C



PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

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1: U74382 **Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete cds** PubMed, Protein, Related Sequences, Taxonomy, OMIM, LinkOut

```
LOCUS       HSU74382     1929 bp    mRNA            PRI       30-SEP-1999
DEFINITION  Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete
            cds.
ACCESSION   U74382
VERSION     U74382.1  GI:2058492
KEYWORDS    telomere protein; telomere maintenance; mitotic regulator;
            NIMA-interacting proteins (Pins); cell cycle regulation.
```

FIG. 13A

FIG. 13A
FIG. 13B
FIG. 13C
FIG. 13D

FIG. 13

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1929)
AUTHORS Lu,K.P., Hanes,S.D. and Hunter,T.
TITLE A human peptidyl-prolyl isomerase essential for regulation of mitosis
JOURNAL Nature 380 (6574), 544-547 (1996)
MEDLINE 96195064
REFERENCE 2 (bases 1 to 1929)
AUTHORS Shen,M., Haggblom,C., Vogt,M., Hunter,T. and Lu,K.P.
TITLE Characterization and cell cycle regulation of the related human telomeric proteins Pin2 and TRF1 suggest a role in mitosis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (25), 13618-13623 (1997)
MEDLINE 98054283
PUBMED 9391075
REFERENCE 3 (bases 1 to 1929)
AUTHORS Lu,K.P. and Hunter,T.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1996) Molecular Biology and Virology Laboratory, Salk Institute, 10010 North Torrey Pines Rd, La Jolla, CA 92037, USA

FEATURES	Location/Qualifiers
source	1..1929
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/cell_line="HeLa"
gene	1..1929
	/gene="PIN2"

FIG. 13B

```
CDS             1..1260
                /gene="PIN2"
                /note="NIMA-interacting protein 2, a potential coordinator
                between mitotic progression and telomere homeostasis"
                /codon_start=1
                /product="telomeric repeat DNA-binding protein"
                /protein_id="AAB53363.1"
                /db_xref="GI:2058493"
                /translation="MAEDVSSAAPSPRRCADGRDADPTEEQMAETERNDEEQFECQEL
                LECQVQVGAPEEEEEEEEDAGLVAEAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRRTR
                NSAEAIIHGLSSLTACQLRTIYICQFLTRIAAGKTLDAQFENDERITPLESALMIWGS
                IEKEHDKLHEEIQNLIKIQAIAVCMENGNFKEAEEVFERIFGDPNSHMPFKSKLLMII
                SQKDTFHSFFQHFSYNHMMEKIKSYVNYVLSEKSSTFLMKAAAKVVESKRTRTITSQD
                KPSGNDVEMETEANLDTRKRSHKNLFLSKLQHGTQQQDLNKKERRVGTPQSTKKKKES
                RRATESRIPVSKSQPVTPEKHRARKRQAWLWEEDKNLRSGVRKYGEGNWSKILLHYKF
                NNRTSVMLKDRWRTMKKLKLISSDSED"
BASE COUNT      618 a    386 c    435 g    490 t
ORIGIN
        1 atggcggagg atgtttcctc agcggccccg agcccgcggc ggtgtgcgga tggtagggat
       61 gccgacccta ctgaggagca gatggcagaa acagagagaa acgacgagga gcagttcgaa
      121 tgccaggaac tgctcgagtg ccaggtgcag gtgggggccc ccgaggagga ggaggaggag
      181 gaggaggacg cgggcctggt ggccgaggcc gaggccgtgg ctgccggctg gatgctcgat
      241 ttcctctgcc tctctctttg ccgagctttc cgcgacggcc gctccgagga cttccgcagg
      301 acccgcaaca gcgcagaggc tattattcat ggactatcca gtctaacagc ttgccagttg
      361 agaacgatat acatatgtca gtttttgaca agaattgcag caggaaaaac ccttgatgca
      421 cagtttgaaa atgatgaacg aattacaccc ttggaatcag ccctgatgat ttggggttca
      481 attgaaaagg aacatgacaa acttcatgaa gaaatacaga atttaattaa aattcaggct
      541 atagctgttt gtatggaaaa tggcaacttt aaagaagcag aagaagtctt tgaaagaata
      601 tttggtgatc caaattctca tatgcctttc aaaagcaaat tgcttatgat aatctctcag
      661 aaagatacat ttcattcctt ttttcaacac ttcagctaca accacatgat ggagaaaatt
      721 aagagttatg tgaattatgt gctaagtgaa aaatcatcaa cctttctaat gaaggcagcg
      781 gcaaaagtag tagaaagcaa aaggacaaga acaataactt ctcaagataa acctagtggt
```

FIG. 13C

```
 841 aatgatgttg aaatggaaac tgaagctaat ttggatacaa gaaaaaggtc tcacaagaat
 901 cttttcttat ctaagttgca acatggaacc cagcaacaag accttaataa gaaagaaaga
 961 agagtaggaa ctcctcaaag tacaaaaaag aaaaaagaaa gcagaagagc cactgaaagc
1021 agaatacctg tttcaaagag tcagccggta actcctgaaa aacatcgagc tagaaaaaga
1081 caggcatggc tttgggaaga agacaagaat ttgagatctg gcgtgaggaa atatggagag
1141 ggaaactggt ctaaaatact gttgcattat aaattcaaca accggacaag tgtcatgtta
1201 aaagacagat ggaggaccat gaagaaacta aaactgattt cctcagacag cgaagactga
1261 ttgtgtttgt aaaagcttga tgaaaggaca gttaagtatt ttgatcactg cattttgttt
1321 gaaacttgtg tcattgatgt aatttaaaac ttttgtttaa agcattacag tatttttctg
1381 tgaccatcaa ttaatgaggg tttgtgctac cagagttaaa gcatatgcta tcattgtatt
1441 ctttaagaac cttatttga taaaatgtaa atttgttgaa ccctgccaca tttagtatcc
1501 ccacccccaa atcctgttcc aatgaaaaaa ttaaaacctg atacgaaaaa aaaaaaattc
1561 cagttaacct attttgtgtc tgtaggctga cctcaaccct gtaacgtaac ccattaaaat
1621 gaatttcttt ttttttaaga cagagtttct ctctgttgcc caggctggag tgcagtggcg
1681 caatttcagc tcactgaacc tctgcctccc aggtcaagtg attctcctgc ctcagcctct
1741 gagtagctgg gattacaggc acacaccacc agccagctaa tttttgtatt tttagtagag
1801 gcggggtttc accatgctgg tcaggatgtt ctccaactcc tgacttcatg atccacccac
1861 ctcggcctcc caaagtgctg agattacaga cgtgagccac tgcgtcctgc ctaaaatgaa
1921 ttttctaga
```


FIG. 13D